# Dot Plot *IMG 2.9*

## Introduction

**Dotplot** is a tool for comparing the sequences of two genomes. **Dotplot** employs the program **Mummer** to generate dotplot diagrams between two genomes. It uses input DNA sequences directly for comparing genomes with similar sequences (NUCmer). It uses the six frame amino acid translation of the DNA input sequences (PROmer) for comparing genomes with dissimilar sequences (because the DNA sequence is not as highly conserved as the amino acid translation).



**Figure 1**. Select 2 genomes for Dot Plot

**Dotplot** can be applied on two genomes that are selected from the list of all available or preselected genomes (Figure 1). Select which **algorithm** to use (nucleotide based comparison for genomes with similar nucleotide sequences or protein base comparison for genomes with dissimilar nucleotide sequences), and select the genome that will be used as **reference**.
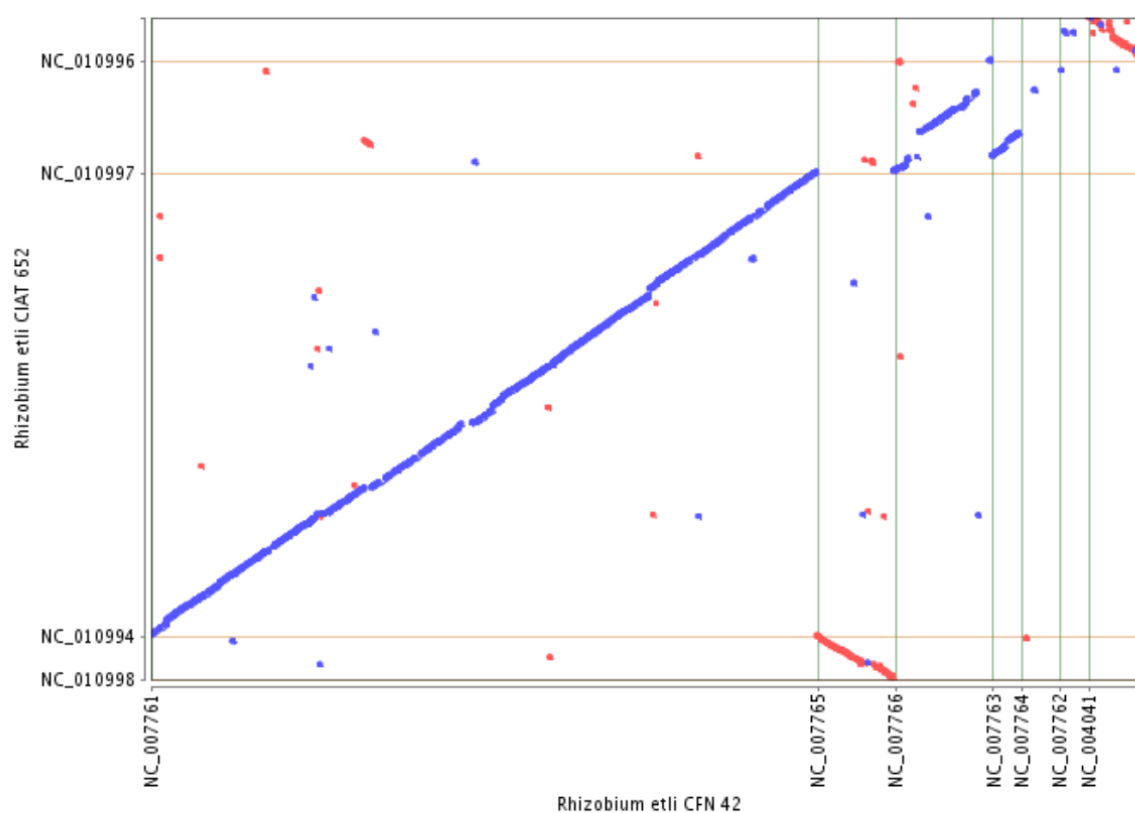
**Figure 2**. Dot Plot – fplot (blue), rplot (red)

The dotplot (Figure 2) consists of **blue** points for regions of similarity found on parallel strands (fplot) and **red** points for regions of similarity found on antiparallel strands (rplot). The tooltip for each point shows which plot it is and the coordinates and scaffolds of the alignment. Clicking on a point brings up the chromosomal neighborhood of the alignment of the two genomes (Figure 3). The plot can be saved either as PDF or as TIFF.
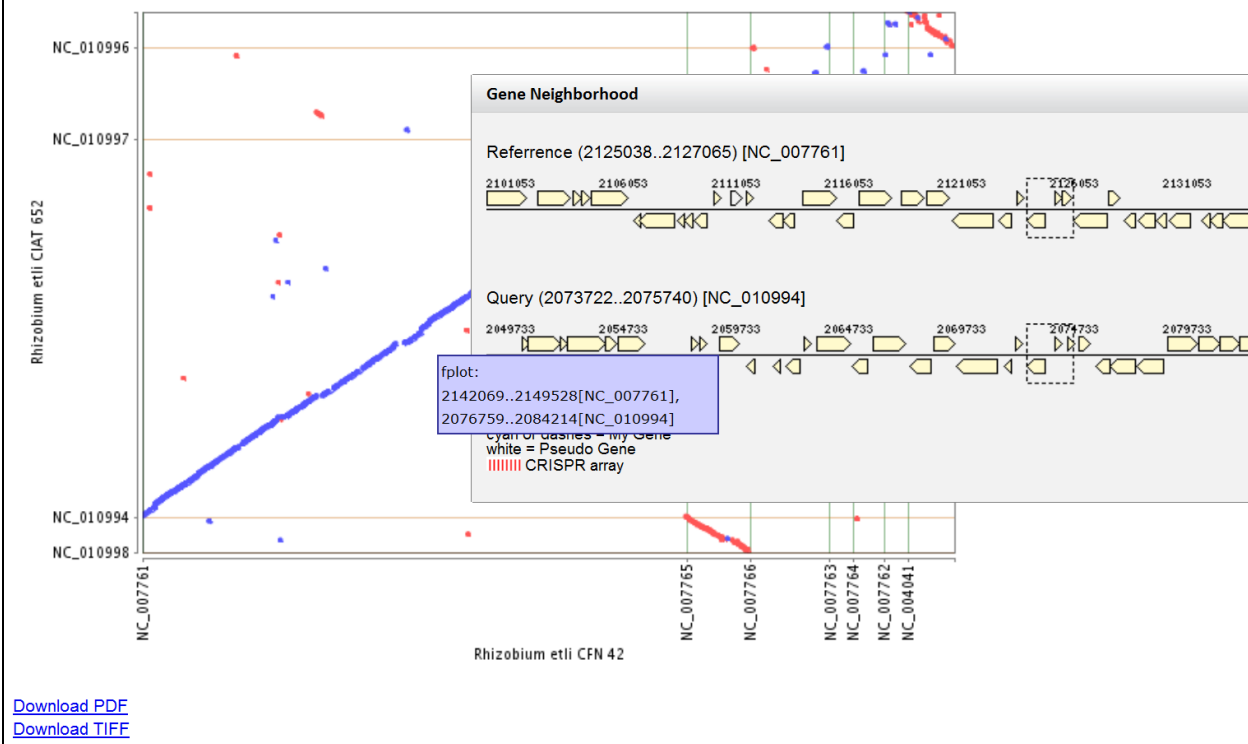
**Figure 3**. Dot Plot – tooltips, links to Gene Neighborhood of aligned region

# Scaffold Selection <span style="color:orange">*IMG 3.3*</span>

When the number of scaffolds for the 2 genomes selected for Dot Plot is too high, the computation of the Dot Plot may time out. In such a scenario, the user is offered a choice to select a subset of scaffolds or to continue with the calculation using all scaffolds (Figure 5). The current cutoff is when the number of scaffold is >150 for both genomes or >300 for one of the genomes
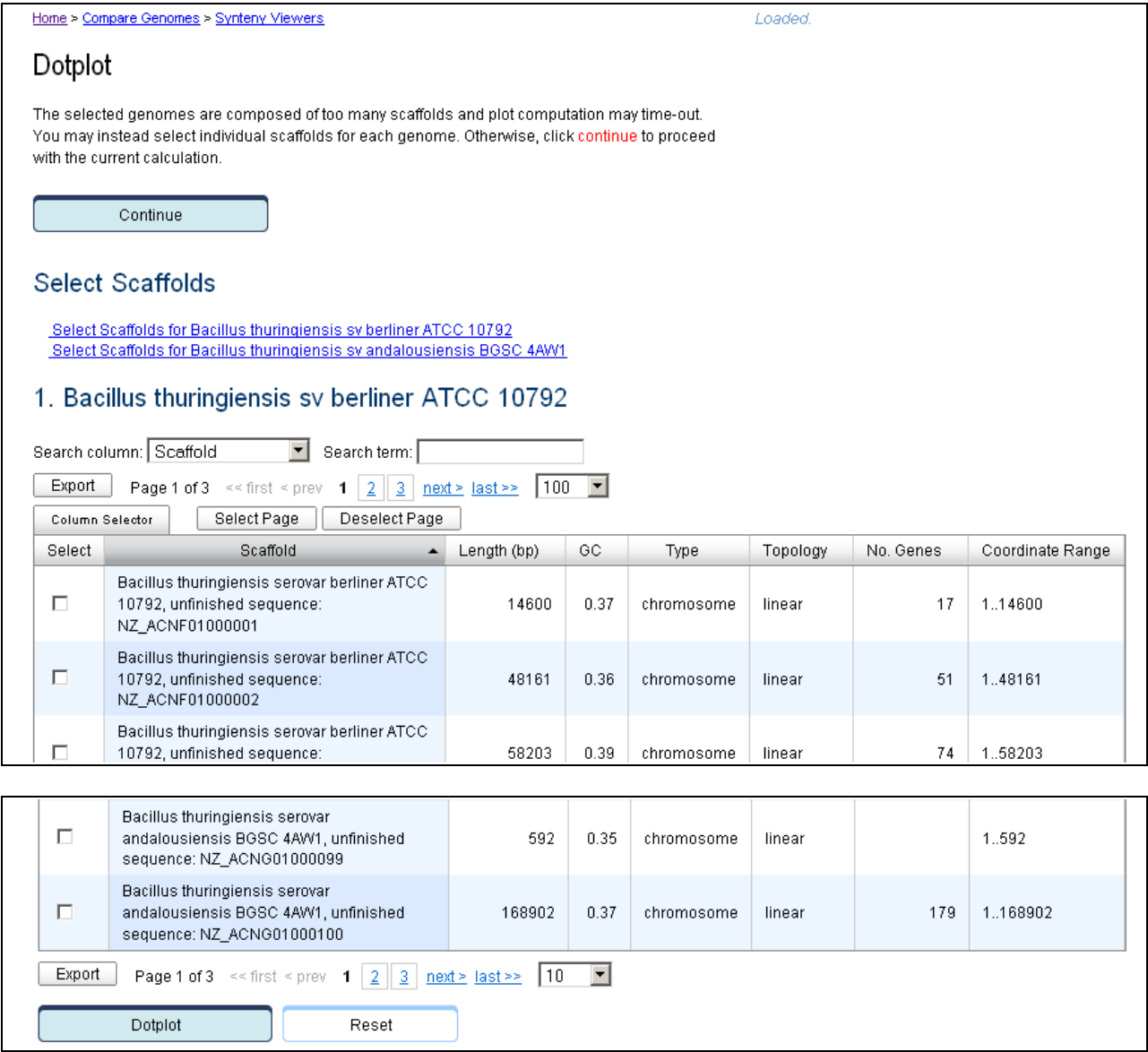


**Figure 5**. Select Scaffolds for Dot Plot